

## Abstract

**Background:** Human adenoviruses (HAdVs) are common pathogens associated with diseases affecting the respiratory tract, gastro intestinal tract as well as various organs like the liver, kidney and the brain. Currently there are 60 human adenovirus serotypes classified into 7 species A to G on the basis of serology, genome sequencing and phylogenomics. HAdV species B, C and E are mainly implicated in respiratory tract infections whereas the other species are associated with gastrointestinal, genitourinary, and ocular infections. Globally, the respiratory HAdV species play a significant role in pediatric infections accounting for 10% of overall respiratory illnesses and 5%–11% of pneumonia cases. However the disease burden due to respiratory adenoviruses in Kenya is not well studied; there is limited data on the respiratory human adenovirus species and serotypes circulating in the country.

**Objective:** The aim of this study was to characterize respiratory human adenoviruses using serological and molecular approaches. Specifically the study sought to determine the species and serotypes of HAdVs that were associated with pediatric respiratory infections in New Nyanza Provincial General Hospital from June 2010 to June 2012.

**Methods:** Respiratory human adenoviruses isolated from patient's samples in a period of two years were characterized using serological and molecular approaches. Virus isolates in Hep-2 cell cultures were tested with specific fluorescent antibodies to confirm the presence of Human adenovirus. The loop-2 fragment of the hexon gene was PCR amplified and then sequenced using the Sanger method.

**Results:** Phylogenomics analysis of the sequences showed that during the study period, respiratory HAdV species B and C were associated with respiratory infections accounting for approximately 1% of the overall respiratory viruses. There were no cases of infections caused by respiratory HAdV E implying that this species was not in circulation during the study period. HAdV C was the predominant species accounting for 68.75% of the reported cases with serotype distribution as HAdV C1-25%, HAdV C2-25%, HAdV C5-6.25%, and HAdV C6-12.5%. HAdV B serotype 7 was the most prevalent serotype at 31.25%. Analysis of selection pressure of the sequences revealed that HAdV C5 and HAdV B7 were under positive selection pressure indicating that these viruses are undergoing an evolutionary process which signifies instability in their genomes.

**Conclusions:** Characterization of respiratory human adenoviruses that circulated at New Nyanza Provincial General hospital during the study period revealed that species B and C were present but not E. There was significant genetic variation in the hexon gene of the HAdVs seen at this site compared to those from other parts of the world implying continuing evolution of respiratory HAdVs. To gain a complete understanding of this evolutionary process, whole genome sequencing of these viruses is called for in order to determine genetic stability and uniqueness of these viruses